DT05 Rec'd PCT/PTO 18 OCT 2004

SEQUENCE LISTING

<110> Lynkeus Biotech GmbH

<120> Means and Methods for the Specific Modulation of Target Genes in the CNS and the Eye and Methods for Their Identification

- <130> LY01A04/P-WO
- <150> EP02008761.5
- <151> 2002-04-18
- <150> US 60/431,173
- <151> 2002-12-05
- <160> 10
- <170> PatentIn version 3.1
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- <212> DNA
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Ala Tyr Thr Ser Glu Glu Ser Glu Asn Glu Asn Pro His Ala Arg Gly 50 55

Ser Phe Ser Tyr Lys Ser Leu Arg Lys Gly Gly Pro Ser Gln Arg Glu 75

Gln Tyr Leu Pro Gly Ala Ile Ala Ile Phe Asn Val Asn Asn Ser Ser 85

Asn Lys Asp Gln Glu Pro Glu Glu Lys Lys Lys Lys Lys Glu Lys

Lys Ser Lys Ser Asp Asp Lys Asn Glu Asn Lys Asn Asp Pro Glu Lys

Lys Lys Lys Lys Lys Lys Lys Lys Lys Glu Glu Lys Ser 130 135

Lys Asp Lys Lys Glu His His Lys Lys Glu Val Val Val Ile Asp Pro 145

Ser Gly Asn Thr Tyr Tyr Asn Trp Leu Phe Cys Ile Thr Leu Pro Val

Met Tyr Asn Trp Thr Met Val Ile Ala Arg Ala Cys Phe Asp Glu Leu

Gln Ser Asp Tyr Leu Glu Tyr Trp Leu Ile Leu Asp Tyr Val Ser Asp 205 200 195

Ile Val Tyr Leu Ile Asp Met Phe Val Arg Thr Arg Thr Gly Tyr Leu 215 220 210

Glu Gln Gly Leu Leu Val Lys Glu Glu Leu Lys Leu Ile Asn Lys Tyr

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225 230 235 240

Lys Ser Asn Leu Gln Phe Lys Leu Asp Val Leu Ser Leu Ile Pro Thr 245 250 255

Asp Leu Leu Tyr Phe Lys Leu Gly Trp Asn Tyr Pro Glu Ile Arg Leu 260 265 270

Asn Arg Leu Leu Arg Phe Ser Arg Met Phe Glu Phe Phe Gln Arg Thr 275 280 285

Glu Thr Arg Thr Asn Tyr Pro Asn Ile Phe Arg Ile Ser Asn Leu Val 290 295 300

Met Tyr Ile Val Ile Ile Ile His Trp Asn Ala Cys Val Phe Tyr Ser 305 310 315

Ile Ser Lys Ala Ile Gly Phe Gly Asn Asp Thr Trp Val Tyr Pro Asp 325 330 335

Ile Asn Asp Pro Glu Phe Gly Arg Leu Ala Arg Lys Tyr Val Tyr Ser 340 345 350

Leu Tyr Trp Ser Thr Leu Thr Leu Thr Thr Ile Gly Glu Thr Pro Pro 355 360 365

Pro Val Arg Asp Ser Glu Tyr Val Phe Val Val Asp Phe Leu Ile 370 375 380

Gly Val Leu Ile Phe Ala Thr Ile Val Gly Asn Ile Gly Ser Met Ile 385 390 395 400

Ser Asn Met Asn Ala Ala Arg Ala Glu Phe Gln Ala Arg Ile Asp Ala 405 410 415

Ile Lys Gln Tyr Met His Phe Arg Asn Val Ser Lys Asp Met Glu Lys 420 425 430

Arg Val Ile Lys Trp Phe Asp Tyr Leu Trp Thr Asn Lys Lys Thr Val 435 440 445

Asp Glu Lys Glu Val Leu Lys Tyr Leu Pro Asp Lys Leu Arg Ala Glu 450 455 460

Ile Ala Ile Asn Val His Leu Asp Thr Leu Lys Lys Val Arg Ile Phe 465 470 475 480

Ala Asp Cys Glu Ala Gly Leu Leu Val Glu Leu Val Leu Lys Leu Gln
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Pro Gln Val Tyr Ser Pro Gly Asp Tyr Ile Cys Lys Lys Gly Asp Ile 500 505 510

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Gly Glu Ile Ser Ile Leu Asn Ile Lys Gly Ser Lys Ala Gly Asn Arg 545 550 555 560

Arg Thr Ala Asn Ile Lys Ser Ile Gly Tyr Ser Asp Leu Phe Cys Leu 565 570 575

Ser Lys Asp Asp Leu Met Glu Ala Leu Thr Glu Tyr Pro Asp Ala Lys 580 585 590

Thr Met Leu Glu Glu Lys Gly Lys Gln Ile Leu Met Lys Asp Gly Leu 595 600 605

Leu Asp Leu Asn Ile Ala Asn Ala Gly Ser Asp Pro Lys Asp Leu Glu 610 615 620

Glu Lys Val Thr Arg Met Glu Gly Ser Val Asp Leu Leu Gln Thr Arg 625 630 635 640

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gtg gtc ttc aag gtc ctg Val Val Phe Lys Val Leu 75 80	cgg cgc ctc Arg Arg Leu	tgc acc ctc ctg (Cys Thr Leu Leu (85	cag gcc gac 291 Gln Ala Asp 90
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gcc acc agg ctt ttc agc Ala Thr Arg Leu Phe Ser 110	gtg cag ccg Val Gln Pro 115	Asp Ser Val Leu	gag gac tgc 387 Glu Asp Cys 120
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gtg ggc cac gtg gct cag Val Gly His Val Ala Gln 140	acc aaa aag Thr Lys Lys 145	atg gtg aac gtc Met Val Asn Val 150	gag gac gtg 483 Glu Asp Val
gcc gag tgc cct cac ttc Ala Glu Cys Pro His Phe 155	Ser Ser Phe	gct gac gag ctc Ala Asp Glu Leu 165	act gac tac 531 Thr Asp Tyr 170
aag aca aag aat atg ctg Lys Thr Lys Asn Met Leu 175	gcc aca ccc Ala Thr Pro	atc atg aat ggc Ile Mét Asn Gly 180	aaa gac gtc 579 Lys Asp Val 185

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His Trp Ala Leu Ala Ser Gly Leu Pro Ser Tyr Val Ala Glu Ser Gly 340 345 350

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Lys Leu Lys Ser Tyr Tyr Thr Asp Leu Glu Ala Phe Ala Met Val Thr 580 585 590

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